

SEQUENCE LISTING

<110> Genentech, Inc. Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.

RECEIVED

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TECH CENTER 1600/2900

<120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same

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<150> PCT/US00/04414

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<151> 1999-07-07

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Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
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Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
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Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
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Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser 515 520 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala 530 535 540

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Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly 580 585 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln 595 600

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu 610 615 620

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Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu

335

340 345 350

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn 360 Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr 375 Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys 395 400 Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu 405 Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe 425 Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu 440 Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser 455 Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys 475 Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu 500 505 Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp 545 550 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly 570 Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys 580 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser 610 Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile 640 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser 690 695 700

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Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly 740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu 770 775 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser 850 855 860

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Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val Glu Gly Gly Val
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Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
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Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
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Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val
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Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr
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Leu Glu Leu Asn Val Leu Val Pro Pro Ala Pro Pro Ser Cys Arg Leu
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                                        155
Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
                165
                                    170
                                                        175
Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
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Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
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Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu 230 235 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly 250 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His 265 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp 280 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile 295 Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg 310 305 Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser 330 Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly 345 Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser 360 355 Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser 380 375 Gln Ala Gly Ser Leu Val 390 385 <210> 40 <211> 22 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 40 22 agggtctcca ggagaaagac tc <210> 41 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic

oligonucleotide probe

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caaactgcca tttagataat gtctgtatag ctgcaaatat taataaaact ttaacaaaaa 420
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taaggtettg tgcaagagga geeetegete ttetgtteet teteggeace acetggatet 1920
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Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly
Ser Tyr Tyr Cys Met Cys Val Pro Gly Phe Arg Ser Ser Ser Asn Gln
Asp Arg Phe Ile Thr Asn Asp Gly Thr Val Cys Ile Glu Asn Val Asn
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                               105
Ala Asn Cys His Leu Asp Asn Val Cys Ile Ala Ala Asn Ile Asn Lys
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Thr Leu Thr Lys Ile Arg Ser Ile Lys Glu Pro Val Ala Leu Leu Gln
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Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
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Thr Tyr Ile Glu Ile Leu Ala Glu Ser Ser Leu Leu Gly Tyr Lys
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485 490 495

Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly 500 505 510

Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe 515 520 525

Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val 530 535 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys 545 550 555 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu 610 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln 660 665 670

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Leu Arg 690

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<220>

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aatcacctga cacattttgc aattttgatg teetetggte ettecattgg tattaaagat 480
tataatattc ttacaaggat cactcaacta ggaataatta tttcactgat ttqtcttqcc 540
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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
                                        75
Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
                               105
Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
                           120
Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
    130
                       135
Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
                   150
                                       155
Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
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ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140

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Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
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Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
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Val Arg Ser Pro Ser Phe Glu Lys
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                        215
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                                                                   22
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Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly 85 90 95

Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu 115 120 125

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Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro 405 410 415

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Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
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Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
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Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
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Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
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120

125

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Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu His Cys Glu Gly 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser 305 310 315 320

Pro Val Pro Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys 355 360 365

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- Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe 50 55 60
- Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn 65 70 75 80
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- Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr 165 170 175
- Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu 180 185 190
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- Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys 210 215 220
- Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val 225 230 235 240
- Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr 245 250 255
- Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro 260 265 270
- Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr 275 280 285
- Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala 290 295 300

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Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln

345

305

315

350

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Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu
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Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val
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<211> 2026
<212> DNA
<213> Homo sapiens
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ageogagege eggtgtgage cagegetget gecagtgtga geggeggtgt gagegeggtg 240
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<212> PRT
<213> Homo sapiens
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Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
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Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
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Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
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Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
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130 135 140

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<210> 107
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<211> 1838
<212> DNA
<213> Homo sapiens
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qqttatcqct qcatctqtqc cgagggctac aagcagatgg aaggcatctg tgtgaaggag 1140
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<213> Homo sapiens
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         35
                             40
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Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
                                         75
Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
                                105
Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
        115
                            120
Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
145
                    150
                                        155
                                                             160
Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
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Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
                                185
Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
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200

205

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Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys 245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg 260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg 275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu 290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln 305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr 325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala 340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln 355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys 370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met 385 390 395 400

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Ile Lys Gly Arg 420

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<212> DNA

<213> Artificial Sequence

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<210> 111

<211> 22

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<400> 113
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<211> 366

<212> PRT

<213> Homo sapiens

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Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu 20 25 30

Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met 35 40 45

Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu 50 55 60

Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln 65 70 75 80

Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr 85 90 95

His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu 100 105 110

Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala 115 120 125

Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg 130 135 140

Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr 145 150 155 160

Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys 165 170 175

Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg 180 185 190

Pro Arg Gln Pro Leu Leu Gln Val Ser Val Gln Arg Glu His Leu 195 200 205

Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln 210 215 220

Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu 225 230 235 240

Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro 245 250 255

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<213> Homo sapiens
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Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
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                                                  45
Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
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                         55
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Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe 85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val 115 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro 145 150 155 160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 120

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gcctggaggc cgccgcgagc ccgctttcca ccccgacctc tgcccaggcc gcaggcccca 180
geteaggete gtgeeeacee accaagttee agtgeegeae eagtggetta tgegtgeeee 240
teacetggeg etgegaeagg gaettggaet geagegatgg eagegatgag gaggagtgea 300
ggattgagee atgtaceeag aaagggeaat geecacegee eeetggeete eeetgeeeet 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
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ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
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teacetetet caggaatgee acaaceatgg ggeeeeetgt gaceetggag agtgteeeet 660
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aagttgcttc
<210> 127
<211> 282
<212> PRT
<213> Homo sapiens
<400> 127
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Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
         35
                             40
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
                         55
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
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                     70
                                         75
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
                 85
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
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<400> 125

100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Leu Arg Asn Cys Ser 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln \$245\$ \$250\$ \$255\$

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<400> 128

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24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<2205

<400> 129

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<210> 130
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<210> 131
<211> 1843
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<213> Homo sapiens
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<222> (1837)..(1837)
<223> a, t, c or g
<400> 131
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cagactettg caagetggat geeetetgtg gatgaaagat gtateatgga atgaaceega 180
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cgggcgggtt cgatgacctt caagtgtgtg ctgaccccgg cattcccgag aatggcttca 360
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gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatcg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaatc atcacttgtc 600
atgaaggatt caagatccgg taccccgacc tacacaatat ggtttcatta tgtcgcgatg 660
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gttgatctgt ggagttgatt cctttccttc tcttggtttt agacaaatgt aaacaaagct 1740
ctgatcctta aaattgctat gctgatagag tggtgagggc tggaagcttg atcaagtcct 1800
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<210> 132
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<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

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Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val 20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr 35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu 50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val 65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser 100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu 115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile 130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn 145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile 165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn 180 185 190

Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr 195 200 205

Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys 210 215 220

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu 225 230 235 240

Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe

Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val 260 265 270

Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr 275 280 285

Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys 290 295 300

Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr 305 310 315 320

Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu 325 330 335

Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His $340 \hspace{1.5cm} 345 \hspace{1.5cm} 350$

Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe 355 360 365

Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala 370 375 380

Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val 385 390 395 400

Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr 405 410 415

Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys
420 425 430

Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro
435 440 445

Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile 450 455 460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

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<210> 134

<211> 23

<212> DNA

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      oligonucleotide probe
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                                                                  23
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<211> 1815
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<213> Homo sapiens
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ggccttgtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
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cggacctaga ggtctacaat gtcataagaa aacaaagcga agctgactta gctgagaccc 1080
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<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

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Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro 35 40 45

Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe 50 55 60

Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser 65 70 75 80

Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn 85 90 95

Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Glu
100 105 110

Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr 115 120 125

Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser 130 135 140

Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro 145 150 155 160

Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys 165 170 175

Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala 180 185 190

Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro 195 200 205

Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys 210 215 220

Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser 225 230 235 240

Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val 245 250 255

Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys

			260					265					270					
Lys	Gln	His 275	Thr	Ile	Trp	Pro	Ser 280	Pro	His	Gln	Gly	Asn 285	Ser	Pro	Asp			
Leu	Glu 290	Val	Tyr	Asn	Val	Ile 295	Arg	Lys	Gln	Ser	Glu 300	Ala	Asp	Leu	Ala			
Glu 305	Thr	Arg	Pro	Asp	Leu 310	Lys	Asn	Ile	Ser	Phe 315	Arg	Val	Cys	Ser	Gly 320			
Glu	Ala	Thr	Pro	Asp 325	Asp	Met	Ser	Cys	Asp 330	Tyr	Asp	Asn	Met	Ala 335	Val			
Asn	Pro	Ser	Glu 340	Ser	Gly	Phe	Val	Thr 345	Leu	Val	Ser	Val	Glu 350	Ser	Gly			
Phe	Val	Thr 355	Asn	Asp	Ile	Tyr	Glu 360	Phe	Ser	Pro	Asp	Gln 365	Met	Gly	Arg			
Ser	Lys 370	Glu	Ser	Gly	Trp	Val 375	Glu	Asn	Glu	Ile	Tyr 380	Gly	Tyr					
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<213 <213	0> 14 1> 24 2> Di 3> Ai	4	icial	l Sed	quenc	ce												
<220 <220	3> De	escr: ligo:					cial	Seq	uence	e: S	ynthe	etic					-	
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65

70

Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu

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<211> 1514
<212> DNA
<213> Homo sapiens
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cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
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cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720
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attectecae atectagaga geaacetget gaaageeatg gaetetgeea etgeeeeega 1140
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<210> 142
<211> 428
<212> PRT
<213> Homo sapiens
<400> 142
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                                 25
Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
Lys Leu Lys Met Val Gln Val Val Phe Arq His Gly Ala Arg Ser Pro
                         55
Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
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Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
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                     70
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Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu 85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr 210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg 225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu 245 250 255

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Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
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Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
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Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
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Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met 245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile 260 265 270

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Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
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Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
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Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
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215

220

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Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His 260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu 275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr 290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys 305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro 325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly 340 345 350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His 435 440 445

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Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
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Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly

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- Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr 435 440 445
- Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn 450 455 460
- Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr 465 470 475 480
- Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly 485 490 495
- Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val 500 510
- Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys 515 520 525
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Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
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Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser 165 170 175

Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val 180 185 190

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Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser 225 230 235 240

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Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn 260 265 270

Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys 275 280 285

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Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys 195 200 205

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Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys 290 295 300

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Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile 325 330 335

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Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
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Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys

75

70

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- Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe 100 105 110
- Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr 115 120 125
- Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser 130 135 140
- Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp 145 150 155 160
- Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg 165 170 175
- Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu 180 185 190
- Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys 195 200 205
- Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val 210 215 220
- Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser 225 230 230 235 235
- Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly 260 265 270
- Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro 275 280 285
- His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr 290 295 300
- Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val 305 310 315 320
- Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn 325 330 335
- Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg 340 345 350
- Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr 355 360 365
- Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val 370 375 380

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Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala 65 70 75 80

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Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr 145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser 165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser 180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu 195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala 210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu 225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe 245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn

260 265 270

Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala 280 Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro 290 295 Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala 305 310 315 Glu Val <210> 202 <211> 24 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 202 24 gagettteca tecaggtgte atge <210> 203 <211> 22 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 203 22 gtcagtgaca gtacctactc gg <210> 204 <211> 24 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 204 24 tggagcagga ggagtagtag tagg <210> 205 <211> 50 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic

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Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg 50 55 60

Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn 65 70 75 80

Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val 145 150 155 160

Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile 165 170 175

Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly 180 185 190

Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg 225 230 235 240

Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn 245 250 255

Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp

260 265 270

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- His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
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- Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu 65 70 75 80
- Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
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- Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg 100 105 110
- His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp 115 120 125
- Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly 130 135 140
- His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr 145 150 155 160
- Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp 165 170 175
- Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu 180 185 190
- His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr 195 200 205
- Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu 210 215 220
- Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala 225 230 235 240
- Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn 245 250 255
- Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro $260 \hspace{1.5cm} 265 \hspace{1.5cm} 270 \hspace{1.5cm}$
- Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu 275 280 285
- Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly 290 295 300
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Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser 450 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met 500 505 510

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn 35 40 45

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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys
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Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
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Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser 130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln 145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met 165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp 180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys 195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220

Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240

Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255

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Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe 95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu 110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His 125 130 135

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Val	Ile	Arg	Trp	Ala 380	Asn	Ala	Thr	Gly	Thr 385	Arg	Val	Arg	Phe	Ile 390
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Leu	Pro	Leu	Ile	Ser 425	Pro	Arg	Ser	Phe	Pro 430	Pro	Ser	Leu	Gln	Val 435

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Lys	Glu	Ala	Thr	Ser 620	Cys	His	Arg	Ala	Leu 625	Gly	Asp	Arg	Pro	Gly 630
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Ala	Pro	Ser	Val	Arg 680	Val	Val	Ser	Ala	Pro 685	Leu	Val	Leu	Pro	Trp 690
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Cys Thr Val Asp Ile Glu Ser Leu Thr Gly Tyr Arg Thr Tyr Arg 35 40 45

Cys Ala His Pro Leu Ala Thr Leu Phe Lys Ile Leu Ala Ser Phe $50 \\ \hspace{1.5cm} 55 \\ \hspace{1.5cm} 60$

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Ser Ile Arg Glu Glu Ser Ser Tyr Ser Asp Ile Pro Asp Val Lys 95 100 105

Asn Asp Phe Ala Phe Met Leu His Leu Ile Asp Gln Tyr Asp Pro 110 115 120

Leu Tyr Ser Lys Arg Phe Ala Val Phe Leu Ser Glu Val Ser Glu 125 130 135

Asn Lys Leu Arg Gln Leu Asn Leu Asn Asn Glu Trp Thr Leu Asp 140 145 150

Lys Leu Arg Gln Arg Leu Thr Lys Asn Ala Gln Asp Lys Leu Glu 155 160 165

Leu His Leu Phe Met Leu Ser Gly Ile Pro Asp Thr Val Phe Asp 170 175 180

Leu Val Glu Leu Glu Val Leu Lys Leu Glu Leu Ile Pro Asp Val 185 190 195

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Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala

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Arg	Lys	Asp	Ala	Tyr 50	Met	Phe	Trp	Trp	Leu 55	Tyr	Tyr	Ala	Thr	Asn 60
Ser	Cys	Lys	Asn	Phe 65	Ser	Glu	Leu	Pro	Leu 70	Val	Met	Trp	Leu	Gln 75
Gly	Gly	Pro	Gly	Gly 80	Ser	Ser	Thr	Gly	Phe 85	Gly	Asn	Phe	Glu	Glu 90
Ile	Gly	Pro	Leu	Asp 95	Ser	Asp	Leu	Lys	Pro 100	Arg	Lys	Thr	Thr	Trp 105
Leu	Gln	Ala	Ala	Ser 110	Leu	Leu	Phe	Val	Asp 115	Asn	Pro	Val	Gly	Thr 120
Gly	Phe	Ser	Tyr	Val 125	Asn	Gly	Ser	Gly	Ala 130	Tyr	Ala	Lys	Asp	Leu 135
Ala	Met	Val	Ala	Ser 140	Asp	Met	Met	Val	Leu 145	Leu	Lys	Thr	Phe	Phe 150
Ser	Cys	His	Lys	Glu 155	Phe	Gln	Thr	Val	Pro 160	Phe	Tyr	Ile	Phe	Ser 165
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Tyr	Lys	Ala	Ile	Gln 185	Arg	Gly	Thr	Ile	Lys 190	Cys	Asn	Phe	Ala	Gly 195
Val	Ala	Leu	Gly	Asp 200	Ser	Trp	Ile	Ser	Pro 205	Val	Asp	Ser	Val	Leu 210
Ser	Trp	Gly	Pro	Tyr 215	Leu	Tyr	Ser	Met	Ser 220	Leu	Leu	Glu	Asp	Lys 225
Gly	Leu	Ala	Glu	Val 230	Ser	Lys	Val	Ala	Glu 235	Gln	Val	Leu	Asn	Ala 240

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Ala	Glu	Met	Ile	Ile 260	Glu	Gln	Asn	Thr	Asp 265	Gly	Val	Asn	Phe	Tyr 270
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Leu	Glu	Phe	Thr	Gln 290	Ser	His	Leu	Val	Cys 295	Leu	Cys	Gln	Arg	His 300
Val	Arg	His	Leu	Gln 305	Arg	Asp	Ala	Leu	Ser 310	Gln	Leu	Met	Asn	Gly 315
Pro	Ile	Arg	Lys	Lys 320	Leu	Lys	Ile	Ile	Pro 325	Glu	Asp	Gln	Ser	Trp 330
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Met	Lys	Pro	Val	Ile 350	Ser	Ile	Val	Asp	Glu 355	Leu	Leu	Glu	Ala	Gly 360
Ile	Asn	Val	Thr	Val 365	Tyr	Asn	Gly	Gln	Leu 370	Asp	Leu	Ile	Val	Asp 375
Thr	Met	Gly	Gln	Glu 380	Ala	Trp	Val	Arg	Lys 385	Leu	Lys	Trp	Pro	Glu 390
Leu	Pro	Lys	Phe	Ser 395	Gln	Leu	Lys	Trp	Lys 400	Ala	Leu	Tyr	Ser	Asp 405
Pro	Lys	Ser	Leu	Glu 410	Thr	Ser	Ala	Phe	Val 415	Lys	Ser	Tyr	Lys	Asn 420
Leu	Ala	Phe	Tyr	Trp 425	Ile	Leu	Lys	Ala	Gly 430	His	Met	Val	Pro	Ser 435
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Gln Glu

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<211> 1100

<212> DNA

<213> Homo Sapien

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Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly 35 40 45

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Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg

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<211> 314

<212> PRT

<213> Homo Sapien

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Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser $95 \hspace{1.5cm} 100 \hspace{1.5cm} 105$

Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe 110 115 120

Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro 125 130 135

Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
140 145 150

Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
155 160 165

Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys 170 175 180

Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln 185 190 195

Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys 200 205 210

Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly 215 220 225

Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly 230 235 240

Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val 245 250 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
260 265 270

Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met \$275\$ 280 285

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Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val 305

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<212> DNA

<213> Homo Sapien

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<211> 556

<212> PRT

<213> Homo Sapien

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Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
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Thr	Cys	Trp	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130		Leu	Leu	Pro	Gly 135		
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Val	Arg	Ser	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165		
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Ser	Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195		
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Ala	Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240		
Ala	Gln	Phe	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255		
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Gln	Glu	Pro	Phe	Leu 305	Gln	Trp	Leu	Met	Leu 310	Leu	Ser	Asn	Glu	Ser 315		
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Pro	Thr	Phe	Pro	Ala 380	Ser	Ser	Pro	Tyr	Val 385	Thr	Thr	Val	Gly	Gly 390
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Tyr	Ile	Ser	Gly	Gly 410	Gly	Phe	Ser	Asn	Val 415	Phe	Pro	Arg	Pro	Ser 420
Tyr	Gln	Glu	Glu	Ala 425	Val	Thr	Lys	Phe	Leu 430	Ser	Ser	Ser	Pro	His 435
Leu	Pro	Pro	Ser	Ser 440	Tyr	Phe	Asn	Ala	Ser 445	Gly	Arg	Ala	Tyr	Pro 450
Asp	Val	Ala	Ala	Leu 455	Ser	Asp	Gly	Tyr	Trp 460	Val	Val	Ser	Asn	Arg 465
Val	Pro	Ile	Pro	Trp 470	Val	Ser	Gly	Thr	Ser 475	Ala	Ser	Thr	Pro	Val 480
Phe	Gly	Gly	Ile	Leu 485	Ser	Leu	Ile	Asn	Glu 490	His	Arg	Ile	Leu	Ser 495
Gly	Arg	Pro	Pro	Leu 500	Gly	Phe	Leu	Asn	Pro 505	Arg	Leu	Tyr	Gln	Gln 510
His	Gly	Ala	Gly	Leu 515	Phe	Asp	Val	Thr	Arg 520	Gly	Cys	His	Glu	Ser 525
Cys	Leu	Asp	Glu	Glu 530	Val	Glu	Gly	Gln	Gly 535	Phe	Cys	Ser	Gly	Pro 540
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Thr	Trp	Pro	Ala	Tyr 35		Leu	Pro	Val	Val 40		Pro	Gln	Ser	Th:
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Val	Ser	Ser	Ser	Cys 65		Pro	Gln	Cys	His 70		Gly	Thr	Pro	Leu 75
Pro	Thr	Tyr	Glu	Glu 80	Ala	Lys	Gln	Tyr	Leu 85	Ser	Tyr	Glu	Thr	Leu 90
Tyr	Ala	Asn	Gly	Ser 95	Arg	Thr	Glu	Thr	Gln 100	Val	Gly	Ile	Tyr	
_	_													105
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Ser	Gly	Lys	Ser	Arg 125	Arg	Lys	Arg	Gln	Ile 130	Tyr	Gly	Tyr	Asp	Ser 135
Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Cys	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240

Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro 245 His Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys 265 Gln Leu Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu 290 Thr Tyr Asp Leu Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala 305 310 Ser Gly Ser Gly Val Tyr Val Arg Met Trp Lys Arg Gln Gln 325 Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe Ser Gly His Gln Trp 335 Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn Val Ala Val Arg 360 355 350 Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp Ile Lys Gly 370

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<211> 1378

<212> DNA

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<213> Homo Sapien

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caggatacet gtteececag eetgtgggaa geeceageag etgaaeceggg 200
ttgtgggegg egaggacage actgaeageg agtggeettg gategtgage 250
atecagaaga atgggaecea eeactgegea ggttetetge teaecageeg 300
etgggtgate actgetgee actgtteaa ggacaaecetg aacaaaecat 350
acetgttete tgtgetgetg ggggeetgge agetgggaa eeetgggtet 400
eggteecaga aggtggtgt tgeetgggtg gageeceaec etgtgtatte 450

ctggaaggaa ggtgcctgtg cagacattgc cctggtgcgt ctcgagcgct 500

ccatacagtt ctcagagcgg gtcctgccca tctgcctacc tgatgcctct 550 atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650 ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700 ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850 geogagegea acaggeoegg ggtetacate ageotetetg egeacegete 900 ctqqqtqqaq aaqatcqtqc aaqqqqtqca qctccqcggg cgcgctcagg 950 ggggtggggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000 tectagggeg cagegggaeg egggetegg atetgaaagg eggeeagate 1050 cacatetgga tetggatetg eggeggeete gggeggttte eeeegeegta 1100 aataggetea tetaeeteta eetetggggg eeeggaegge tgetgeggaa 1150 aggaaacccc ctccccgacc cgcccgacgg cctcaggccc ccctccaagg 1200 catcaggccc cgcccaacgg cetcatgtcc ccgccccac gacttccggc 1250 cccgccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350 ataaattatt tattctccaa aaaaaaaa 1378

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<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

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Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu 20 25 30

Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln $35 \hspace{1cm} 40 \hspace{1cm} 45$

Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu
50 55 60

Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys
65 70 75

Ala	Gly	Ser	Leu	Leu 80	Thr	Ser	Arg	Trp	Val 85	Ile	Thr	Ala	Ala	His 90
Cys	Phe	Lys	Asp	Asn 95	Leu	Asn	Lys	Pro	Tyr 100	Leu	Phe	Ser	Val	Leu 105
Leu	Gly	Ala	Trp	Gln 110	Leu	Gly	Asn	Pro	Gly 115	Ser	Arg	Ser	Gln	Lys 120
Val	Gly	Val	Ala	Trp 125	Val	Glu	Pro	His	Pro 130	Val	Tyr	Ser	Trp	Lys 135
Glu	Gly	Ala	Cys	Ala 140	Asp	Ile	Ala	Leu	Val 145	Arg	Leu	Glu	Arg	Ser 150
Ile	Gln	Phe	Ser	Glu 155	Arg	Val	Leu	Pro	Ile 160	Cys	Leu	Pro	Asp	Ala 165
Ser	Ile	His	Leu	Pro 170	Pro	Asn	Thr	His	Cys 175	Trp	Ile	Ser	Gly	Trp 180
Gly	Ser	Ile	Gln	Asp 185	Gly	Val	Pro	Leu	Pro 190	His	Pro	Gln	Thr	Leu 195
Gln	Lys	Leu	Lys	Val 200	Pro	Ile	Ile	Asp	Ser 205	Glu	Val	Cys	Ser	His 210
Leu	Tyr	Trp	Arg	Gly 215	Ala	Gly	Gln	Gly	Pro 220	Ile	Thr	Glu	Asp	Met 225
Leu	Cys	Ala	Gly	Tyr 230	Leu	Glu	Gly	Glu	Arg 235	Asp	Ala	Cys	Leu	Gly 240
Asp	Ser	Gly	Gly	Pro 245	Leu	Met	Cys	Gln	Val 250	Asp	Gly	Ala	Trp	Leu 255
Leu	Ala	Gly	Ile	Ile 260	Ser	Trp	Gly	Glu	Gly 265	Cys	Ala	Glu	Arg	Asn 270
Arg	Pro	Gly	Val	Tyr 275	Ile	Ser	Leu	Ser	Ala 280	His	Arg	Ser	Trp	Val 285
Glu	Lys	Ile	Val	Gln 290	Gly	Val	Gln	Leu	Arg 295	Gly	Arg	Ala	Gln	Gly 300
Gly	Gly	Ala	Leu	Arg 305	Ala	Pro	Ser	Gln	Gly 310	Ser	Gly	Ala	Ala	Ala 315

Arg Ser

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<213> Artificial Sequence

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<210> 265
<211> 19
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 265
gcagaggtgt ctaaggttg 19
<210> 266
<211> 24
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<400> 266
agetetagae caatgeeage ttee 24
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<400> 270
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<400> 271
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<211> 18
<212> DNA
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<223> Synthetic Oligonucleotide Probe
<400> 272
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 <400> 273
 tactgggtgg tcagcaac 18
 <210> 274
 <211> 24
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<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence
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<400> 276
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<210> 277
<211> 18
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<223> Synthetic Oligonucleotide Probe
<400> 277
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tgacaatgac cgaccagg 18
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<400> 281
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<211> 61
<212> DNA
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 tgccaggtgg a 61
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 atgctgtgtg ccggctact 119
<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien
<400> 284
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<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

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Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala 35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val 65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Gly Glu Asn Leu Phe 80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu 95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys 110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala 125 130 135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu 140 145 150

Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr 155 160 165

Glu Pro P	ro Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr Pro C	ys Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Cys	Lys	Asn	Ser 195
Leu Cys G	lu Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr Leu V	al Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp Ser A	rg Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
Pro Ala Pl	he Leu	Val 245	Thr	Glu	Val	Ser	Gly 250	Ser	Leu	Ala	Thr	Lys 255
Ala Leu P	ro Ala	Val 260	Glu	Thr	Gln	Ala	Pro 265	Thr	Ser	Leu	Ala	Thr 270
Lys Asp P	ro Pro	Ser 275	Met	Ala	Thr	Glu	Ala 280	Pro	Pro	Cys	Val	Thr 285
Thr Glu Va	al Pro	Ser 290	Ile	Leu	Ala	Ala	His 295	Ser	Leu	Pro	Ser	Leu 300
Asp Glu G	lu Pro	Val 305	Thr	Phe	Pro	Lys	Ser 310	Thr	His	Val	Pro	Ile 315
Pro Lys S	er Ala	Asp 320	Lys	Val	Thr	Asp	Lys 325	Thr	Lys	Val	Pro	Ser 330
Arg Ser P	ro Glu	Asn 335	Ser	Leu	Asp	Pro	Lys 340	Met	Ser	Leu	Thr	Gly 345
Ala Arg G	lu Leu	Leu 350	Pro	His	Ala	Gln	Glu 355	Glu	Ala	Glu	Ala	Glu 360
Ala Glu L	eu Pro	Pro 365	Ser	Ser	Glu	Val	Leu 370	Ala	Ser	Val	Phe	Pro 375
Ala Gln A	sp Lys	Pro 380	.Gly	Glu	Leu	Gln	Ala 385	Thr	Leu	Asp	His	Thr 390
Gly His T	hr Ser	Ser 395	Lys	Ser	Leu	Pro	Asn 400	Phe	Pro	Asn	Thr	Ser 405
Ala Thr A	la Asn	Ala 410	Thr	Gly	Gly	Arg	Ala 415	Leu	Ala	Leu	Gln	Ser 420
Ser Leu P	ro Gly	Ala 425	Glu	Gly	Pro	Asp	Lys 430	Pro	Ser	Val	Val	Ser 435
Gly Leu A	sn Ser	Gly 440	Pro	Gly	His	Val	Trp 445	Gly	Pro	Leu	Leu	Gly 450

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<400> 286
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<400> 287
 ctcatattgc acaccagtaa ttcg 24
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 ctttttcaca ttagcagacc ggacttaagt cacaacagat tatctttcat 150
 caaggcaagt tocatgagcc accttcaaag ccttcgagaa gtgaaactga 200
 acaacaatga attggagacc attccaaatc tgggaccagt ctcggcaaat 250
 attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300
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acatctgaaa gagtttcagt cccttgaaac tttggacctt agcagcaaca 350

atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400

tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450 tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500 ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550 aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600 tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650 atggagettt ttgggggetg ageaacatgg aaattttgca getggaecat 700 aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750 gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800 cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850 ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900 actgcacatt gggaacaaca gagtcagcta cattgctgat tgtgccttcc 950 gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000 tggactattg aagacatgaa tggtgctttc tctgggcttg acaaactgag 1050 gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100 tcactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150 atgtetttae aaggeaatge atttteacaa atgaagaaac tgeaacaatt 1200 gcatttaaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250 cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350 tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450 gccagcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550 gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgaggtggaa 1600 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700 ccaagacccc catggatete accatecgag etggggeeat ggeaegettg 1750 gagtgtgctg ctgtggggca cccagccccc cagatagcct ggcagaagga 1800

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<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
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Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
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Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu 65 70 75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu 80 85 90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro 95 100 105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr 110 115 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu 125 130 135

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys 140 145 150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp

Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala

410

415

420

				440					445					450		
Ile	Lys	Gly	Ser	Asn 455	Leu	Ser	Phe	Ile	Cys 460	Ser	Ala	Ala	Ser	Ser 465		
Ser	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu		
				470					475					480		
Leu	His	Asp	Ala	Glu 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495		
Gly	Gly	Glu	Val	Met 500	Glu	Tyr	Thr	Thr	Ile 505	Leu	Arg	Leu	Arg	Glu 510		
Val	Glu	Phe	Ala	Ser 515	Glu	Gly	Lys	Tyr	Gln 520	Cys	Val	Ile	Ser	Asn 525		
His	Phe	Gly	Ser	Ser 530	Tyr	Ser	Val	Lys	Ala 535	Lys	Leu	Thr	Val	Asn 540		
Met	Leu	Pro	Ser	Phe 545	Thr	Lys	Thr	Pro	Met 550	Asp	Leu	Thr	Ile	Arg 555		
Ala 、	Gly	Ala	Met	Ala 560	Arg	Leu	Glu	Cys	Ala 565	Ala	Val	Gly	His	Pro 570		
Ala	Pro	Gln	Ile	Ala 575	Trp	Gln	Lys	Asp	Gly 580	Gly	Thr	Asp	Phe	Pro 585		
Ala	Ala	Arg	Glu	Arg 590	Arg	Met	His	Val	Met 595	Pro	Glu	Asp	Asp	Val 600		
Phe	Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	Asp 610	Ile	Gly	Val	Tyr	Ser 615		
Cys	Thr	Ala	Gln	Asn 620	Ser	Ala	Gly	Ser	Ile 625	Ser	Ala	Asn	Ala	Thr 630		
Leu	Thr	Val	Leu	Glu 635	Thr	Pro	Ser	Phe	Leu 640	Arg	Pro	Leu	Leu	Asp 645		
Arg	Thr	Val	Thr	Lys 650	Gly	Glu	Thr	Ala	Val 655	Leu	Gln	Cys	Ile	Ala 660		
Gly	Gly	Ser	Pro	Pro 665	Pro	Lys	Leu	Asn	Trp 670	Thr	Lys	Asp	Asp	Ser 675		
Pro	Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690		
Leu	Leu	Ile	Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705		
Thr	Cys	Glu	Met	Ser 710	Asn	Thr	Leu	Gly	Thr 715	Glu	Arg	Gly	Asn	Val 720		

•

Arg	Leu	Ser	Val	Ile 725	Pro	Thr	Pro	Thr	Cys 730	Asp	Ser	Pro	Gln	Met 735
Thr	Ala	Pro	Ser	Leu 740	Asp	Asp	Asp	Gly	Trp 745	Ala	Thr	Val	Gly	Val 750
Val	Ile	Ile	Ala	Val 755	Val	Cys	Cys	Val	Val 760	Gly	Thr	Ser	Leu	Val 765
Trp	Val	Val	Ile	Ile 770	Tyr	His	Thr	Arg	Arg 775	Arg	Asn	Glu	Asp	Cys 780
Ser	Ile	Thr	Asn	Thr	Asp	Glu	Thr	Asn	Leu	Pro	Ala	Asp	Ile	Pro
				785					790					795
Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810
Tyr	Val	Ser	Ser	Glu 815	Ser	Gly	Ser	His	His 820	Gln	Phe	Val	Thr	Ser 825
Ser	Gly	Ala	Gly	Phe 830	Phe	Leu	Pro	Gln	His 835	Asp	Ser	Ser	Gly	Thr 840
Cys	His	Ile	Asp	Asn 845	Ser	Ser	Glu	Ala	Asp 850	Val	Glu	Ala	Ala	Thr 855
Asp	Leu	Phe	Leu	Cys 860	Pro	Phe	Leu	Gly	Ser 865	Thr	Gly	Pro	Met	Tyr 870
Leu	Lys	Gly	Asn	Val 875	Tyr	Gly	Ser	Asp	Pro 880	Phe	Glu	Thr	Tyr	His 885
Thr	Gly	Cys	Ser	Pro 890	Asp	Pro	Arg	Thr	Val 895	Leu	Met	Asp	His	Tyr 900
Glu	Pro	Ser	Tyr	Ile 905	Lys	Lys	Lys	Glu	Cys 910	Tyr	Pro	Cys	Ser	His 915
Pro	Ser	Glu	Glu	Ser 920	Cys	Glu	Arg	Ser	Phe 925	Ser	Asn	Ile	Ser	Trp 930
Pro	Ser	His	Val	Arg 935	Lys	Leu	Leu	Asn	Thr 940	Ser	Tyr	Ser	His	Asn 945
Glu	Gly	Pro	Gly	Met 950	Lys	Asn	Leu	Cys	Leu 955	Asn	Lys	Ser	Ser	Leu 960
Asp	Phe	Ser	Ala	Asn 965		Glu	Pro	Ala	Ser 970	Val	Ala	Ser	Ser	Asn 975
Ser	Phe	Met	Gly	Thr 980		Gly	Lys	Ala	Leu 985	Arg	Arg	Pro	His	Leu 990
Asp	Ala	Tyr	Ser	Ser 995		Gly	Gln		Ser 1000	Asp	Cys	Gln	Pro	Arg 1005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1010 1015 1020

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn $1025 \hspace{1cm} 1030 \hspace{1cm} 1035$

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro $1040 \hspace{1cm} 1045 \hspace{1cm} 1050 \hspace{1cm}$

Asn Phe Gln Ser Tyr Asp Leu Asp Thr 1055

<210> 291

<211> 2906

<212> DNA

<213> Homo Sapien

<400> 291

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln 35 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser 65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile 80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu 95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe 110 115 120

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg 125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu

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Tyr i	Ala	Phe	Asn	Arg 170	Ile	Pro	Ser	Leu	Arg 175	Arg	Leu	Asp	Leu	Gly 180
Glu 1	Leu	Lys	Arg	Leu 185	Ser	Tyr	Ile	Ser	Glu 190	Gly	Ala	Phe	Glu	Gly 195
Leu S	Ser	Asn	Leu	Arg 200	Tyr	Leu	Asn	Leu	Ala 205	Met	Cys	Asn	Leu	Arg 210
Glu :	Ile	Pro	Asn	Leu 215	Thr	Pro	Leu	Ile	Lys 220	Leu	Asp	Glu	Leu	Asp 225
Leu S	Ser	Gly	Asn	His 230	Leu	Ser	Ala	Ile	Arg 235	Pro	Gly	Ser	Phe	Gln 240
Gly 1	Leu	Met	His	Leu 245	Gln	Lys	Leu	Trp	Met 250	Ile	Gln	Ser	Gln	Ile 255
Gln '	Val	Ile	Glu	Arg 260	Asn	Ala	Phe	Asp	Asn 265	Leu	Gln	Ser	Leu	Val 270
Glu :	Ile	Asn _,	Leu	Ala 275	His	Asn	Asn	Leu	Thr 280	Leu	Leu	Pro	His	Asp 285
Leu l	Phe	Thr	Pro	Leu 290	His	His	Leu	Glu	Arg 295	Ile	His	Leu	His	His 300
Asn 1	Pro	Trp	Asn	Cys 305	Asn	Cys	Asp	Ile	Leu 310	Trp	Leu	Ser	Trp	Trp 315
Ile 1	Lys	Asp	Met	Ala 320	Pro	Ser	Asn	Thr	Ala 325	Cys	Cys	Ala	Arg	Cys 330
Asn :	Thr	Pro	Pro	Asn 335	Leu	Lys	_	Arg	-		Gly	Glu	Leu	Asp 345
Gln A	Asn	Tyr	Phe	Thr 350	Cys	Tyr	Ala	Pro	Val 355	Ile	Val	Glu	Pro	Pro 360
Ala A	Asp	Leu	Asn	Val 365	Thr	Glu	Gly	Met	Ala 370	Ala	Glu	Leu	Lys	Cys 375
Arg A	Ala	Ser	Thr	Ser 380	Leu	Thr	Ser	Val	Ser 385	Trp	Ile	Thr	Pro	Asn 390
Gly :	Thr	Val	Met	Thr 395	His	Gly	Ala	Tyr	Lys 400	Val	Arg	Ile	Ala	Val 405
Leu S	Ser	Asp	Gly	Thr 410	Leu	Asn	Phe	Thr	Asn 415	Val	Thr	Val	Gln	Asp 420
Thr (Gly	Met	Tyr	Thr	Cys	Met	Val	Ser	Asn	Ser	Val	Gly	Asn	Thr

Thr Ala Ser Ala Thr Leu Asn Val Thr Ala Ala Thr Thr Pro 440 445 Phe Ser Tyr Phe Ser Thr Val Thr Val Glu Thr Met Glu Pro Ser 455 460 Gln Asp Glu Ala Arg Thr Thr Asp Asn Asn Val Gly Pro Thr Pro 470 Val Val Asp Trp Glu Thr Thr Asn Val Thr Thr Ser Leu Thr Pro 485 490 Gln Ser Thr Arg Ser Thr Glu Lys Thr Phe Thr Ile Pro Val Thr 500 505 Asp Ile Asn Ser Gly Ile Pro Gly Ile Asp Glu Val Met Lys Thr 515 Thr Lys Ile Ile Ile Gly Cys Phe Val Ala Ile Thr Leu Met Ala 530 535 Ala Val Met Leu Val Ile Phe Tyr Lys Met Arg Lys Gln His His 545 550 555 Arg Gln Asn His His Ala Pro Thr Arg Thr Val Glu Ile Ile Asn 560 565 Val Asp Asp Glu Ile Thr Gly Asp Thr Pro Met Glu Ser His Leu 575 580 Pro Met Pro Ala Ile Glu His Glu His Leu Asn His Tyr Asn Ser 590 595 Tyr Lys Ser Pro Phe Asn His Thr Thr Thr Val Asn Thr Ile Asn 605 610 Ser Ile His Ser Ser Val His Glu Pro Leu Leu Ile Arg Met Asn 620 625 Ser Lys Asp Asn Val Gln Glu Thr Gln Ile 635 <210> 293

430

435

425

<211> 4053

<212> DNA

<213> Homo Sapien

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<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg

Pro	Cys	Pro	Thr	Thr 50	Суѕ	Arg	Cys	Leu	Gly 55	Asp	Leu	Leu	Asp	Су: 60
Ser	Arg	Lys	Arg	Leu 65	Ala	Arg	Leu	Pro	Glu 70	Pro	Leu	Pro	Ser	Trg 75
Val	Ala	Arg	Leu	Asp 80	Leu	Ser	His	Asn	Arg 85	Leu	Ser	Phe	Ile	Lys 90
Ala	Ser	Ser	Met	Ser 95	His	Leu	Gln	Ser	Leu 100	Arg	Glu	Val	Lys	Leu 105
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Ala	Asn	Ile	Thr	Leu 125	Leu	Ser	Leu	Ala	Gly 130	Asn	Arg	Ile	Val	Glu 135
Ile	Leu	Pro	Glu	His 140	Leu	Lys	Glu	Phe	Gln 145	Ser	Leu	Glu	Thr	Le: 15(
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Ala	Leu	Gln	Leu	Lys 170	Tyr	Leu	Tyr	Leu	Asn 175	Ser	Asn	Arg	Val	Th: 180
Ser	Met	Glu	Pro	Gly 185	Tyr	Phe	Asp	Asn	Leu 190	Ala	Asn	Thr	Leu	Let 195
Val	Leu	Lys	Leu	Asn 200	Arg	Asn	Arg	Ile	Ser 205	Ala	Ile	Pro	Pro	Lys 210
Met	Phe	Lys	Leu	Pro 215	Gln	Leu	Gln	His	Leu 220	Glu	Leu	Asn	Arg	Asr 225
Lys	Ile	Lys	Asn	Val 230	Asp	Gly	Leu	Thr	Phe 235	Gln	Gly	Leu	Gly	Ala 240
Leu	Lys	Ser	Leu	Lys 245	Met	Gln	Arg	Asn	Gly 250	Val	Thr	Lys	Leu	Met 255
Asp	Gly	Ala	Phe	Trp 260	Gly	Leu	Ser	Asn	Met 265	Glu	Ile	Leu	Gln	Let 27(
Asp	His	Asn	Asn	Leu 275	Thr	Glu	Ile	Thr	Lys 280	Gly	Trp	Leu	Tyr	Gl ₃ 285
Leu	Leu	Met	Leu	Gln 290	Glu	Leu	His	Leu	Ser 295	Gln	Asn	Ala	Ile	Asr 300
Arg	Ile	Ser	Pro	Asp 305	Ala	Trp	Glu	Phe	Cys 310	Gln	Lys	Leu	Ser	Gli 315
Len	Asp	Len	Thr	Phe	Asp	His	Len	Ser	Ara	Len	Asn	Asp	Ser	Ser

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Arg	Val	Ser	Tyr	Ile 350	Ala	Asp	Cys	Ala	Phe 355	Arg	Gly	Leu	Ser	Ser 360
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Glu	Asp	Met	Asn	Gly 380	Ala	Phe	Ser	Gly	Leu 385	Asp	Lys	Leu	Arg	Arg 390
Leu	Ile	Leu	Gln	Gly 395	Asn	Arg	Ile	Arg	Ser 400	Ile	Thr	Lys	Lys	Ala 405
Phe	Thr	Gly	Leu	Asp 410	Ala	Leu	Glu	His	Leu 415	Asp	Leu	Ser	Asp	Asn 420
Ala	Ile	Met	Ser	Leu 425	Gln	Gly	Asn	Ala	Phe 430	Ser	Gln	Met	Lys	Lys 435
Leu	Gln	Gln	Leu	His 440	Leu	Asn	Thr	Ser	Ser 445	Leu	Leu	Суѕ	Asp	Cys 450
Gln	Leu	Lys	Trp	Leu 455	Pro	Gln	Trp	Val	Ala 460	Glu	Asn	Asn	Phe	Gln 465
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- <212> PRT
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- Gly Val Arg Gly Gln Ala Leu Tyr Leu Pro Val His Tyr Gly Phe 35 40 45
- His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg 50 55 60
- Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser 65 70 75
- Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro $80 \\ 85 \\ 90$
- Pro Asn Ala Ser Leu Leu Ile Asn Pro Leu Gln Phe Pro Asp Glu 95 100 105
- Gly Asn Tyr Ile Val Lys Val Asn Ile Gln Gly Asn Gly Thr Leu 110 115 120
- Ser Ala Ser Gln Lys Ile Gln Val Thr Val Asp Asp Pro Val Thr $125 \hspace{1.5cm} 130 \hspace{1.5cm} 135$
- Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr 140 145 150
- Val Gly Asn Met Thr Leu Thr Cys His Val Glu Gly Gly Thr Arg 155 160 165
- Leu Ala Tyr Gln Trp Leu Lys Asn Gly Arg Pro Val His Thr Ser 170 175 180
- Ser Thr Tyr Ser Phe Ser Pro Gln Asn Asn Thr Leu His Ile Ala 185 190 195
- Pro Val Thr Lys Glu Asp Ile Gly Asn Tyr Ser Cys Leu Val Arg 200 205 210
- Asn Pro Val Ser Glu Met Glu Ser Asp Ile Ile Met Pro Ile Ile

215 220 225 Tyr Tyr Gly Pro Tyr Gly Leu Gln Val Asn Ser Asp Lys Gly Leu 230 235 Lys Val Gly Glu Val Phe Thr Val Asp Leu Gly Glu Ala Ile Leu Phe Asp Cys Ser Ala Asp Ser His Pro Pro Asn Thr Tyr Ser Trp Ile Arg Arg Thr Asp Asn Thr Thr Tyr Ile Ile Lys His Gly Pro 275 Arg Leu Glu Val Ala Ser Glu Lys Val Ala Gln Lys Thr Met Asp Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu 305 Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu 320 325 Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly 335 Ile Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp 350 Lys Lys Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly 370 375 Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His 380 Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro 410 420 Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser Thr Val Tyr Glu Val Ile Gln His Ile Pro Ala Gln Gln Asp His Pro Glu <210> 321 <211> 25 <212> DNA

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Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln 50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp 65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly
80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His
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Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys 110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile 125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser 140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys 155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser 170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu 185 190 195

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Thr	Asp	Leu	Ile	Tyr 35	Ala	Glu	Lys	Glu	Leu 40	Val	Gln	Ser	Leu	Lys 45
Glu	Tyr	Ile	Leu	Val 50	Glu	Glu	Ala	Lys	Leu 55	Ser	Lys	Ile	Lys	Ser 60
Trp	Ala	Asn	Lys	Met 65	Glu	Ala	Leu	Thr	Ser 70	Lys	Ser	Ala	Ala	Asp 75
Ala	Glu	Gly	Tyr	Leu 80	Ala	His	Pro	Val	Asn 85	Ala	Tyr	Lys	Leu	Val 90
Lys	Arg	Leu	Asn	Thr 95	Asp	Trp	Pro	Ala	Leu 100	Glu	Asp	Leu	Val	Leu 105
Gln	Asp	Ser	Ala	Ala 110	Gly	Phe	Ile	Ala	Asn 115	Leu	Ser	Val	Gln	Arg 120
Gln	Phe	Phe	Pro	Thr 125	Asp	Glu	Asp	Glu	Ile 130	Gly	Ala	Ala	Lys	Ala 135
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Ser	Arg	Gly	Glu	Leu 155	Pro	Gly	Thr	Lys	Tyr 160	Gln	Ala	Met	Leu	Ser 165
Val	Asp	Asp	Cys	Phe 170	Gly	Met	Gly	Arg	Ser 175	Ala	Tyr	Asn	Glu	Gly 180
Asp	Tyr	Tyr	His	Thr 185	Val	Leu	Trp	Met	Glu 190	Gln	Val	Leu	Lys	Gln 195
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Ala	Leu	Glu	Leu	Thr 230	Arg	Arg	Leu	Leu	Ser 235	Leu	Asp	Pro	Ser	His 240
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Asp	Glu	Trp	Asp	Ser 335	Pro	His	Ile	Val	Arg 340	Tyr	Tyr	Asp	Val	Met 345
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Ser	Glu	Ile	Glu	Gln 335	Leu	Gln	Ala	Gln	Ile 340	Arg	Asn	Leu	Thr	Val 345
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Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala

230 235 240 Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile 250 245 Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly 295 His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser 305 310 Asp Asn Asp <210> 342 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 342 tccccaagcc gttctagacg cgg 23 <210> 343 <211> 18 <212> DNA <213> Artificial Sequence <223> Synthetic Oligonucleotide Probe <400> 343 ctggttcttc cttgcacg 18 <210> 344 <211> 28 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 344 gcccaaatgc cctaaggcgg tatacccc 28 <210> 345 <211> 50 <212> DNA <213> Artificial Sequence

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 Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
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Pro	Val	Gly	Lys	Met 155	Ala	Thr	Leu	His	Cys 160	Gln	Glu	Ser	Glu	Gly 165
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His	Leu	Asn	Ser	Glu 200	Thr	Gly	Thr	Leu	Val 205	Phe	Thr	Ala	Val	His 210
Lys	Asp	Asp	Ser	Gly 215	Gln	Tyr	Tyr	Cys	Ile 220	Ala	Ser	Asn	Asp	Ala 225
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